

0002244 0000000000

DHFR-EC 10 20 30 40 50 60 70 80 90 100  
 MISLIAALAVDRVIGMENAMPWNLADLAWFKRNTLDKPVIMGRHTWESIGRPLPGRKNIILSSQPGTDORVTWVKSVDIAAACGDVPEIMVIGGRVY 100  
 1122211 11122112211111 11111211221212112 112111  
 310 120 130 140 150 159  
 EQFLPKAQKLYLTHIDAEEVGDTHFPDYEPPDDWESVESEFHDADAQNSHSYCFKILERR 159  
 111211

TRYP 10 20 30 40 50 60 70 80 90 100  
 IVGGYTCGANTVPYQVSLNSGYHFCGGLINSQWVVSAAHCYKSGIQVRLGEDNINNVVEGNEQFISASKSIVHPSYNSNTLNNDIMLIKLSAASLSRV 100  
 11111 11111  
 110 120 130 140 150 160 170 180 190 200  
 ASISLPTSCASAGTQCLISGWNTKSSGTSYDPVLKCLKAPILSDSSCKSAYPGQITSNMFCAGYLEGGKDSQGDGSGPVVCSGKLGIVSWGSGCAQK 200  
 111111111 111111 1112221121111 11222222221

NRPGVYTKVCNVVSWIKQTIASN 210 220  
 122221  
 RNAS 10 20 30 40 50 60 70 80 90 100  
 KETAARKEERQHMDSSSTAASSNYCNQMMKSRNLTCKDRCKPVNTFVHESLADVQAVCSQKNVACKNGQTCYQSYSTMSITDCRETGSSKYPNCAYKTT 100  
 11111111221 2122211 111121

QANKHIIIVACEGNPYVPVHFEDASV 110 120 124  
 1111111 111222211  
 MYGL 10 20 30 40 50 60 70 80 90 100  
 VLSGEGWQLVLHVWAKVEADVAGHGQDILIRLFKSHPETLEKFDREKHLKTEAEMKASEDLKKHGVTVLTALGAILKKRKHHEAELKPLAQSHATKHKIP 100  
 11111 111211221211 111211221121111 11111221 12121

IKYLEFISEATIHVLHSRHPGDFGADAQAGAMNKALELFRKDIAAKYKELGYQG 110 120 130 140 150  
 1122212111 1111211111111

Fig. 2

	10	20	30	40	50	60	70
DHER-HM	VGSLNCIVAVSQNMGIGKNGDLPWPPLRNEFRYFORMTTSSVEGKQNLVIMGKKTWF	SIPEKNRPLKGR					
DHER-EC	SLIAALA	LPADLAWFKRNTLDK	VIMGRHTWESIGRPLPGR				
	3	9	24	38	40		57

	80	90	100	110	120	130	140
DHFR-HM	INLVLSRELKEPPQGAHF	LRSRLDDALKLTEQP	EELANKVDMVWIVGSS	VYK EAMNHPGLKL	FVTRIMQ		
DHFR-EC				MVIGGG		LYLTHI	
				92 97		110 115	

DHFR-BM  
150 160 170 180 186  
DFESDTFFPEIDLEKYKLLPEYPGVLSVQBEKGKIKYKFEVYEKND